

Genetic Expression Profiles of 18 Genes Regulated by the Filamentation MAPK Pathway

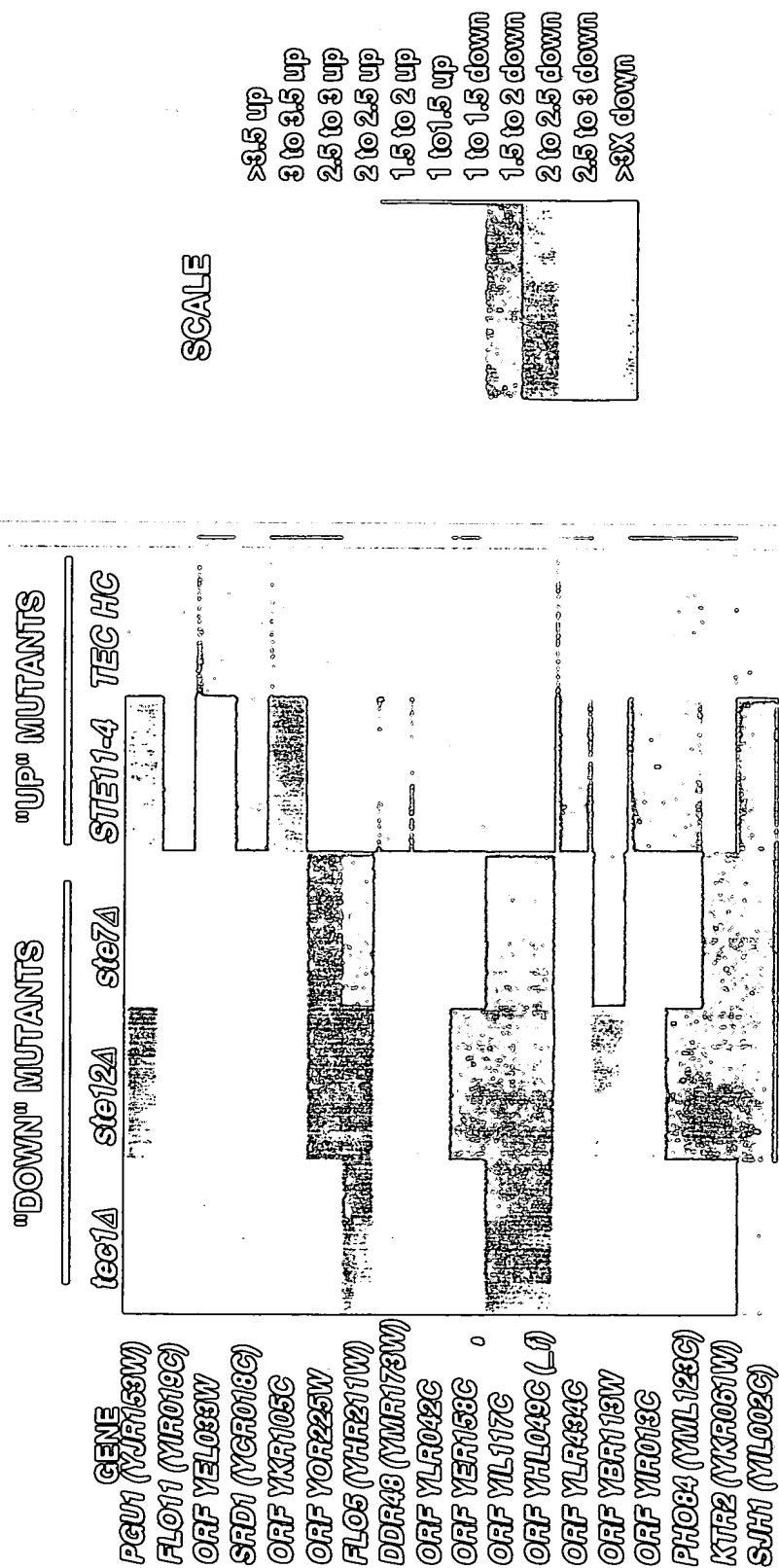


Figure 1

MAPK Targets Include Proteins Known or Predicted to Enter the Secretory Pathway

PGU1	secreted endopolygalacturonase
FLO11	GPI-linked cell surface adhesion factor
TOT10/YEL033W	novel
SRD1	Zinc finger protein
TOT12/YKR105C	putative permease
TOT13/YOR225W	putative membrane protein
FLO5	GPI-linked cell surface adhesion factor
DDR48	cell surface protein
TOT11/YLR042C	GPI-linked cell surface protein
TOT7/YER158C	Homolog of mating morphogenesis protein Afr1
TOT8/YIL117C	Homolog of Chitin Synthase III subunit
TOT20/YHL049C	telomeric protein family member
TOT15/YLR434C	novel
TOT14/YBR113W	putative membrane protein
TOT9/YIR013C	Zinc finger protein
PHO84	phosphate transporter, sugar permease family
KTR2	protein mannosyltransferase homolog
SJH1	Sac1-related inositol phosphate 5-phosphatase homolog

Figure 2

Sytematic Knockout Experiments

GENE	Haploid Invasion	Diploid Filamentation
<i>PGU1</i>	+++	+++
<i>FLO11</i>	-	-
<i>TOT10/YEL033W</i>	+	+
<i>SRD1</i>	ND	ND
<i>TOT12/YKR105C</i>	+++	+++
<i>TOT13/YOR225W</i>	+++	+++
<i>FLO5</i>	+++	+++
<i>DDR48</i>	+++	+++
<i>TOT11/YLR042C</i>	+++	+++
<i>TOT7/YER158C</i>	+++	+++
<i>TOT8/YIL117C</i>	+++	+++
<i>TOT20/YHL049C</i>	ND	ND
<i>TOT15YLR434C</i>	+++	+++
<i>TOT14/YBR113W</i>	+++	+++
<i>TOT9/YIR013C</i>	+++	+++
<i>PHO84</i>	+++	+++
<i>KTR2</i>	+++	+++
<i>SJH1</i>	+++	+++

Figure 3

Filamentation MAPK Pathway Controls Pectinolysis via PGU1

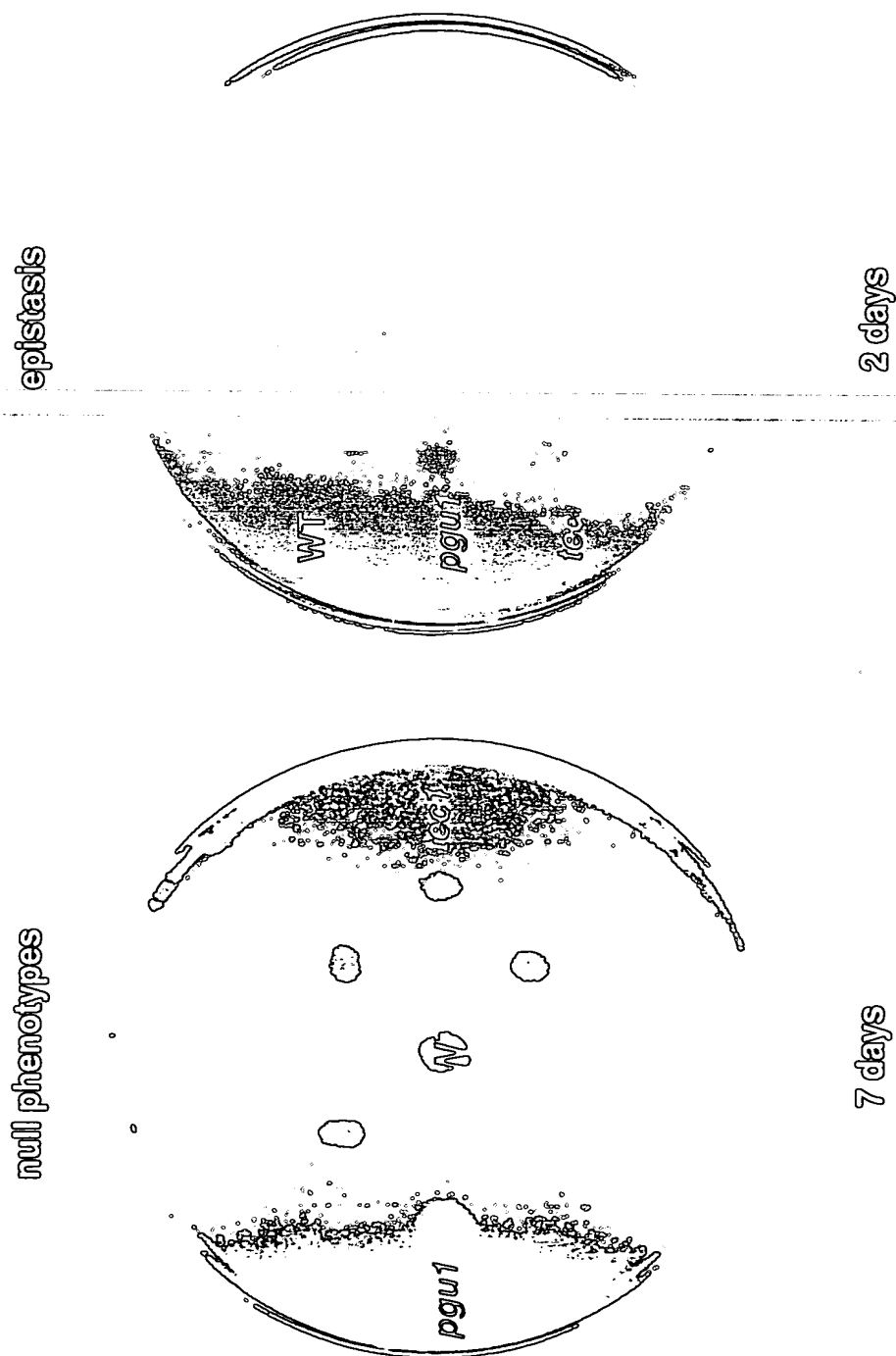


Figure 4

Gene Induction by the Plant-Specific Carbohydrate Polygalacturonic Acid and Its Hydrolysis Product

Genes Selectively Induced by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>XBP1</i>	2.40	6.65	Stress-induced transcriptional repressor
<i>YHR217C</i> (f)	1.30	6.00	Protein of unknown function
<i>YPL080C</i>	2.80	5.70	Protein of unknown function
<i>YPR098C</i>	1.16	5.49	Protein of unknown function
<i>YHL040C</i>	2.04	5.00	Putative MFS Permease
<i>YOL080C</i>	1.35	4.74	Protein with similarity to Rnh70p and Pan2p
<i>PHO84</i>	1.39	4.70	phosphate transport, sugar permease homolog*
<i>YMR293C</i>	1.29	4.07	Protein with similarity to amidase
<i>YLR184W</i>	1.33	3.24	Protein of unknown function
<i>YIL011W</i>	1.01	3.01	Protein with similarity to PAU1 family
<i>CYT1</i>	1.02	2.82	Cytochrome c1
<i>ATP11</i>	1.29	2.65	F1-ATP synthase assembly protein
<i>YOR091W</i>	1.17	2.51	Protein of unknown function
<i>PAU3</i>	1.02	2.46	Stress-induced protein of the PAU1 family
<i>SKO1</i>	0.47	2.35	ATF/CREB transcriptional repressor
<i>MSI4</i>	0.73	2.06	Rab guanine nucleotide dissociation inhibitor
Regulated by Filamentation MAPK Pathway*			

Genes Selectively Induced by Galacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>VPS1</i>	4.03	1.69	Vacuolar sorting protein, dynamin GTPase

Figure 5

Gene Repression by the Plant-Specific Carbohydrate Polygalacturonic Acid and its Hydrolysis Product

Genes Selectively Repressed by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
COP1/SEC33	0.63	0.17	alpha subunit of coatamer complex
YOL002C	1.36	0.18	Protein of unknown function
YDL173W	0.96	0.24	Protein of unknown function
COQ2	1.37	0.25	coenzyme Q (ubiquinone) biosynthesis
YIL176C (f)	0.86	0.30	Protein with similarity to PAU1 family
YFL032W	0.80	0.30	Protein of unknown function
RPS33A	1.10	0.34	Ribosomal protein S28A
ARC35	1.25	0.39	Component of ARP2/3 complex
RPS26A	0.87	0.39	Ribosomal protein S26A
RPS10A	1.02	0.46	Ribosomal protein S10A

Genes Selectively Repressed by Galacturonic Acid

gene	GA/-	PGA/-	Protein Information
YEL033W	0.12	0.38	Protein of unknown function*
VID24	0.24	1.46	Vacuolar import and degradation of Fbp1
NDC1	0.29	1.02	Spindle pole body duplication factor
SKO1	0.47	2.35	ATF/CREB transcriptional repressor

*Regulated by the Filamentation MAPK Pathway

Figure 6

Figure 7

NAME=GA						
gene	YPD	GA	PGA	GA/YPD	PGA/YPD	
ORF YIL101C	20	48	133	2.40	6.65	
ORF YLR344W exon 1 (_i)	33	138	208	4.18	6.30	
ORF YHR217C (_r_i)	20	29	120	1.45	6.00	
ORF YHR217C (_f)	20	26	120	1.30	6.00	
ORF YPL080C	20	56	114	2.80	5.70	
ORF YPR098C	37	43	203	1.16	5.49	
ORF YHL040C	27	55	135	2.04	5.00	
ORF YOL080C	23	31	109	1.35	4.74	
PHO84 (YML123C)	33	46	155	1.39	4.70	
ORF YMR293C	28	36	114	1.29	4.07	
ORF YLR184W	66	88	214	1.33	3.24	
ORF YIL011W	153	154	460	1.01	3.01	
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94	
CYT1 (YOR065W)	91	93	257	1.02	2.82	
ORF YLL025W (_f)	251	355	693	1.41	2.76	
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73	
ATP11 (YNL315C)	51	66	135	1.29	2.65	
ORF YOR091W	59	69	148	1.17	2.51	
ORF YMR143W exon 1 (_i)	385	895	964	2.32	2.50	
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46	
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46	
SKO1 (YNL167C)	43	20	101	0.47	2.35	
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15	
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12	
ORF YNL006W	77	100	161	1.30	2.09	
MSI4 (YOR370C)	63	46	130	0.73	2.06	
ORF YPR139C	91	122	187	1.34	2.05	
SPO15 (YKR001C)	35	141	59	4.03	1.69	
HHO1 (YPL127C)	81	45	135	0.56	1.67	
ILV3 (YJR016C)	119	72	182	0.61	1.53	
ORF YBR105C	82	20	120	0.24	1.46	
LYS4 (YDR234W)	479	244	576	0.51	1.20	
ORF YOR009W	144	310	158	2.15	1.10	
NDC1 (YML031W)	113	33	115	0.29	1.02	
ORF YOL073C	143	180	88	1.26	0.62	
ORF YJL223C (_f)	134	175	81	1.31	0.60	
ORF YMR242C	1170	1227	610	1.05	0.52	
ORF YOR248W (_f)	497	422	239	0.85	0.48	
ORF YPL081W exon 1	159	135	75	0.85	0.47	
ORF YML019W	177	91	82	0.51	0.46	
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46	
ORF YMR050C exon 1 (_f)	374	263	169	0.70	0.45	
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39	
ORF YNR035C	200	249	78	1.25	0.39	
ORF YEL033W	172	20	66	0.12	0.38	
TSL1 (YML100W)	103	20	39	0.19	0.38	
RPS33A (YOR167C) (_f)	1726	1899	589	1.10	0.34	
ORF YFL032W	122	98	37	0.80	0.30	
ORF YIL176C (_f)	115	99	34	0.86	0.30	
COQ2 (YNR041C)	84	115	21	1.37	0.25	
ORF YDL173W	141	136	34	0.96	0.24	
ORF YOL002C	111	151	20	1.36	0.18	
ORF YDL145C	118	74	20	0.63	0.17	
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Figure 8

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PROCESS=filter	GENES=53		DIFF=80		MAX= RAT=2	
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Figure 9

Homologous Genes Induced by Filamentation and Mating MAPK Pathways

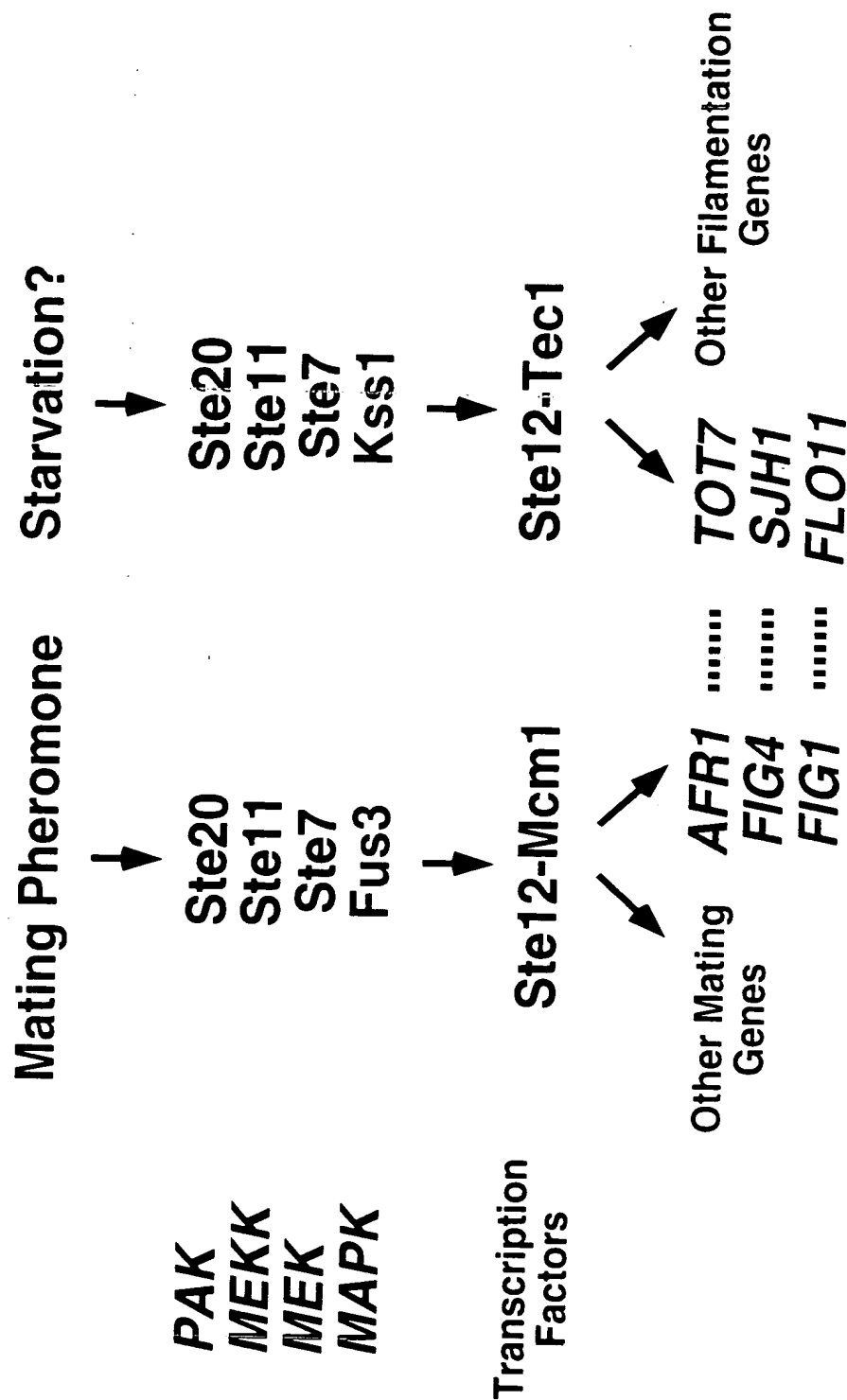


Figure 10

